



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: C. Morrow et al.
- (ii) TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL  
NUCLEIC ACID AND METHODS OF MAKING AND  
USING SAME
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: LAHIVE & COCKFIELD
  - (B) STREET: 28 STATE STREET
  - (C) CITY: BOSTON
  - (D) STATE: MASSACHUSETTS
  - (E) COUNTRY: USA
  - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/756,551
  - (B) FILING DATE: 08-JAN-2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/376,184
  - (B) FILING DATE: 17-AUG-1999
  - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/987,867
  - (B) FILING DATE: 09-DEC-1997
  - (C) CLASSIFICATION:
- (ix) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/389,459
  - (B) FILING DATE: 15-FEB-1995
- (x) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/087,009
  - (B) FILING DATE: 01-JUL-1993
- (xi) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Lauro, Peter C.
  - (B) REGISTRATION NUMBER: 32,360
  - (C) REFERENCE/DOCKET NUMBER: UAI-004CPDV2CN
- (xii) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 227-7400
  - (B) TELEFAX: (617) 742-4214

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATTAGTAGA TCTG

14

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TACAGATGTA CTAA

14

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 845 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 20..845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACACAGCAAT CAGGTCAGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG	52
Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly	
1 5 10	
CAA ATG GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA	100
Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val	
15 20 25	
AAA GTA GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT	148
Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe	
30 35 40	
TCA GCA TTA TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA	196
Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu	
45 50 55	
AAC ACA GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC	244
Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr	
60 65 70 75	
ATC AAT GAG GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA	292

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Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala	
80 85 90	
GGG CCT ATT GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA	340
Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile	
95 100 105	
GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT	388
Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn	
110 115 120	
AAT CCA CCT ATC CCA GTA GGA GAA ATT TAT AAA AGA TGG ATA ATC CTG	436
Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu	
125 130 135	
GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC AGC ATT CTG GAC	484
Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp	
140 145 150 155	
ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC	532
Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe	
160 165 170	
TAT AAA ACT CTA AGA GCC GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG	580
Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp	
175 180 185	
ATG ACA GAA ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACT	628
Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr	
190 195 200	
ATT TTA AAA GCA TTG GGA CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA	676
Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr	
205 210 215	
GCA TGT CAG GGA GTA GGA GGA CCC GGC CAT AAG GCA AGA GTT TTG GCT	724
Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala	
220 225 230 235	
GAA GCA ATG AGC CAA GTA ACA AAT TCA GCT ACC ATA ATG ATG CAG AGA	772
Glu Ala Met Ser Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg	
240 245 250	
GGC AAT TTT AGG AAC CAA AGA AAG ATT GTT AAG TGT TTC AAT TGT GGC	820
Gly Asn Phe Arg Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly	
255 260 265	
AAA GAA GGG CAC ACA GCC AGA AAG T	845
Lys Glu Gly His Thr Ala Arg Lys	
270 275	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His	Gln	1	5	10	15
Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	Glu	20	25	30	
Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	Glu	35	40	45	
Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	50	55	60	
His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	Ala	65	70	75	80
Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	85	90	95	
Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	100	105	110	
Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile	Pro	115	120	125	
Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	130	135	140	
Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	145	150	155	160
Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	Arg	165	170	175	
Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	180	185	190	
Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	Leu	195	200	205	
Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	210	215	220	
Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	Gln	225	230	235	240
Val	Thr	Asn	Ser	Ala	Thr	Ile	Met	Met	Gln	Arg	Gly	Asn	Phe	Arg	Asn	245	250	255	
Gln	Arg	Lys	Ile	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His	Thr	260	265	270	
Ala	Arg	Lys														275			

(2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 4..946

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAC	CAA	TGG	CCA	TTG	ACA	GAA	GAA	AAA	ATA	AAA	GCA	TTA	GTA	GAA	ATT	48
Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile		
1				5					10					15		
TGT	ACA	GAG	ATG	GAA	AAG	GAA	GGG	AAA	ATT	TCA	AAA	ATT	GGG	CCT	GAA	96
Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	
			20						25					30		
AAT	CCA	TAC	AAT	ACT	CCA	GTA	TTT	GCC	ATA	AAG	AAA	AAA	GAC	AGT	ACT	144
Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	
			35					40					45			
AAA	TGG	AGA	AAA	TTA	GTA	GAT	TTC	AGA	GAA	CTT	AAT	AAG	AGA	ACT	CAA	192
Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	
		50					55					60				
GAC	TTC	TGG	GAA	GTT	CAA	TTA	GGA	ATA	CCA	CAT	CCC	GCA	GGG	TTA	AAA	240
Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	
	65					70					75					
AAG	AAA	AAA	TCA	GTA	ACA	GTA	CTG	GAT	GTG	GGT	GAT	GCA	TAT	TTT	TCA	288
Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	
	80				85					90					95	
GTT	CCC	TTA	GAT	GAA	GAC	TTC	AGG	AAG	TAT	ACT	GCA	TTT	ACC	ATA	CCT	336
Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	
			100						105					110		
AGT	ATA	AAC	AAT	GAG	ACA	CCA	GGG	ATT	AGA	TAT	CAG	TAC	AAT	GTG	CTT	384
Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	
			115					120					125			

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CCA CAG GGA TGG AAA GGA TCA CCA GCA ATA TTC CAA AGT AGC ATG ACA Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr 130 135 140	432
AAA ATC TTA GAG CCT TTT AGA AAA CAA AAT CCA GAC ATA GTT ATC TAT Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr 145 150 155	480
CAA TAC ATG GAT GAT TTG TAT GTA GGA TCT GAC TTA GAA ATA GGG CAG Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln 160 165 170 175	528
CAT AGA ACA AAA ATA GAG GAG CTG AGA CAA CAT CTG TTG AGG TGG GGA His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly 180 185 190	576
CTT ACC ACA CCA GAC AAA AAA CAT CAG AAA GAA CCT CCA TTC CTT TGG Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp 195 200 205	624
ATG GGT TAT GAA CTC CAT CCT GAT AAA TGG ACA GTA CAG CCT ATA GTG Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val 210 215 220	672
CTG CCA GAA AAA GAC AGC TGG ACT GTC AAT GAC ATA CAG AAG TTA GTG Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val 225 230 235	720
GGG AAA TTG AAT TGG GCA AGT CAG ATT TAC CCA GGG ATT AAA GTA AGG Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg 240 245 250 255	768
CAA TTA TGT AAA CTC CTT AGA GGA ACC AAA GCA CTA ACA GAA GTA ATA Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile 260 265 270	816
CCA CTA ACA GAA GAA GCA GAG CTA GAA CTG GCA GAA AAC AGA GAG ATT Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile 275 280 285	864
CTA AAA GAA CCA GTA CAT GGA GTG TAT TAT GAC CCA TCA AAA GAC TTA Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu 290 295 300	912
ATA GCA GAA ATA CAG AAG CAG GGG CAA GGC CTCGAG Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly 305 310	948

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys 1 5 10 15
Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn 20 25 30

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Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys  
35 40 45

Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp  
50 55 60

Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys  
65 70 75 80

Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val  
85 90 95

Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser  
100 105 110

Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro  
115 120 125

Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys  
130 135 140

Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln  
145 150 155 160

Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His  
165 170 175

Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu  
180 185 190

Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met  
195 200 205

Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu  
210 215 220

Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly  
225 230 235 240

Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln  
245 250 255

Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro  
260 265 270

Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu  
275 280 285

Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile  
290 295 300

Ala Glu Ile Gln Lys Gln Gly Gln Gly Leu  
305 310

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGGCC TGT CCA AAG GTA TCC TTT GAG CCA ATT CCC ATA CAT TAT TGT	48
Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys	
1 5 10	
GCC CCG GCT GGT TTT GCG ATT CTA AAA TGT AAT AAT AAG ACG TTC AAT	96
Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn	
15 20 25 30	
GGA ACA GGA CCA TGT ACA AAT GTC AGC ACA GTA CAA TGT ACA CAT GGA	144
Gly Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly	
35 40 45	
ATT AGG CCA GTA GTA TCA ACT CAA CTG CTG TTA AAT GGC AGT CTA GCA	192
Ile Arg Pro Val Val Ser Thr Gln Leu Leu Asn Gly Ser Leu Ala	
50 55 60	
GAA GAA GAG GTA GTA ATT AGA TCT GTC AAT TTC ACG GAC AAT GCT AAA	240
Glu Glu Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys	
65 70 75	
ACC ATA ATA GTA CAG CTG AAC ACA TCT GTA GAA ATT AAT TGT ACA AGA	288
Thr Ile Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg	
80 85 90	
CCC AAC AAC AAT ACA AGA AAA AGA ATC CGT ATC CAG AGA GGA CCA GGG	336
Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly	
95 100 105 110	
AGA GCA TTT GTT ACA ATA GGA AAA ATA GGA AAT ATG AGA CAA GCA CAT	384
Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His	
115 120 125	



TGT AAC ATT AGT AGA GCA AAA TGG AAT AAC ACT TTA AAA CAG ATA GAT Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp	432
130 135 140	
AGC AAA TTA AGA GAA CAA TTC GGA AAT AAT AAA ACA ATA ATC TTT AAG Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys	480
145 150 155	
CAA TCC TCA GGA GGG GAC CCA GAA ATT GTA ACG CAC AGT TTT AAT TGT Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys	528
160 165 170	
GGA GGG GAA TTT TTC TAC TGT AAT TCA ACA CAA CTG TTT AAT AGT ACT Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr	576
175 180 185 190	
TGG TTT AAT AGT ACT TGG AGT ACT GAA GGG TCA AAT AAC ACT GAA GGA Trp Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly	624
195 200 205	
AGT GAC ACA ATC ACC CTC CCA TGC AGA ATA AAA CAA ATT ATA AAC ATG Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met	672
210 215 220	
TGG CAG AAA GTA GGA AAA GCA ATG TAT GCC CCT CCC ATC AGT GGA CAA Trp Gln Lys Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln	720
225 230 235	
ATT AGA TGT TCA TCA AAT ATT ACA GGG CTG CTA TTA ACA AGA GAT GGT Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly	768
240 245 250	
GGT AAT AGC AAC AAT GAG TCC GAG ATC TTC AGA CTT GGA GGA GGA GAT Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Leu Gly Gly Gly Asp	816
255 260 265 270	
ATG AGG GAC AAT TGG AGA AGT GAA TTA TAT AAA TAT AAA GTA GTA AAA Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys	864
275 280 285	
ATT GAA CCA TTA GGA GTA GCA CCC ACC AAG GCA AAG AGA AGA GTG GTG Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val	912
290 295 300	
CAG AGA GAA AAA AGA GCA GTG GGA ATA GGA GCT TTG TTC CTT GGG TTC Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe	960
305 310 315	
TTG GGA GCA GCA GGA AGC ACT ATG GGC GCA GCC TCA ATG ACG CTG ACG Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr	1008
320 325 330	
GTA CAG GCC AGA CAA TTA TTG TCT GGT ATA GTG CAG CAG CAG AAC AAT Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn	1056
335 340 345 350	

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TTG CTG AGG GCT ATT GAG GCG CAA CAG CAT CTG TTG CAA CTC ACA GTC Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val 355 360 365	1104
TGG GGC ATC AAG CAG CTC CAA GCA AGA ATC CTA GCT GTG GAA AGA TAC Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr 370 375 380	1152
CTA AAG GAT CAA CAG CTC CTA GGG ATT TGG GGT TGC TCT GGA AAA CTC Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu 385 390 395	1200
ATT TGC ACC ACT GCT GTG CCT TGG AAT GCT AGT TGG AGT AAT AAA TCT Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser 400 405 410	1248
CTG GAA CAG ATC TGG AAT CAC ACG ACC TGG ATG GAG TGG GAC AGA GAA Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu 415 420 425 430	1296
ATT AAC AAT TAC ACA AGC TTA ATA CAC TCC TTA ATT GAA GAA TCG CAA Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln 435 440 445	1344
AAC CAG CAA GAA AAG AAT GAA CAA GAA TTA TTG GAA TTA GAT AAA TGG Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp 450 455 460	1392
GCA AGT TTG TGG AAT TGG TTT AAC ATA ACA AAT TGG CTG TGG TAT ATA Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile 465 470 475	1440
AAA TTA TTC ATA ATG ATA GTA GGA GGC TTG GTA GGT TTA AGA ATA GTT Lys Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val 480 485 490	1488
TTT GCT GTA CTT TCT ATA GTG AAT AGA GTT AGG CAG GGA TAT TCA CCA Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro 495 500 505 510	1536
TTA TCG TTT CAG ACC CAC CTC CCA ATC TCGAG Leu Ser Phe Gln Thr His Leu Pro Ile 515	1568

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 519 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro  
 1 5 10 15  
 Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr  
 20 25 30  
 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg  
 35 40 45  
 Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu  
 50 55 60  
 Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys Thr Ile  
 65 70 75 80  
 Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg Pro Asn  
 85 90 95  
 Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala  
 100 105 110  
 Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn  
 115 120 125  
 Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys  
 130 135 140  
 Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser  
 145 150 155 160  
 Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly  
 165 170 175  
 Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe  
 180 185 190  
 Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser Asp  
 195 200 205  
 Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln  
 210 215 220  
 Lys Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg  
 225 230 235 240  
 Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn  
 245 250 255  
 Ser Asn Asn Glu Ser Glu Ile Phe Arg Leu Gly Gly Gly Asp Met Arg  
 260 265 270  
 Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu  
 275 280 285

Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg  
 290 295 300

Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly  
 305 310 315 320

Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln  
 325 330 335

Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu  
 340 345 350

Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly  
 355 360 365

Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys  
 370 375 380

Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys  
 385 390 395 400

Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu  
 405 410 415

Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn  
 420 425 430

Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln  
 435 440 445

Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser  
 450 455 460

Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu  
 465 470 475 480

Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala  
 485 490 495

Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser  
 500 505 510

Phe Gln Thr His Leu Pro Ile  
 515

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CACCCCTCTC CTACGTAACC AAGGATC

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACTGGTCA CCATATTGGT CAAC

24

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGAGAGAT GGGAGCTCGA GCGTC

25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCCTAT ACGTATTGTG

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGTGAATT CCTAATACGA CTCACTATAG GTTAAACAG C

41

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTATCCTG AGCTCCATAT GTGTCGAGCA GTTTTTGGTT TAGCATTG

48

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Lys Asp Leu Thr Thr Tyr Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2220 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGA CCA GCA GAC CAG ACA GTC ACA GCA GCC TTG ACA AAA CGT TCC TGG	48
Arg Pro Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp	
1 5 10 15	
AAC TCA AGC ACT TCT CCA CAG AGG AGG ACA GAG CAG ACA GCA GAG ACC	96
Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr	
20 25 30	
ATG GAG TCT CCC TCG GCC CCT CCC CAC AGA TGG TGC ATC CCC TGG CAG	144
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln	
35 40 45	
AGG CTC CTG CTC ACA GCC TCA CTT CTA ACC TTC TGG AAC CCG CCC ACC	192
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr	
50 55 60	
ACT GCC AAG CTC ACT ATT GAA TCC ACG CCG TTC AAT GTC GCA GAG GGG	240
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly	
65 70 75 80	
AAG GAG GTG CTT CTA CTT GTC CAC AAT CTG CCC CAG CAT CTT TTT GGC	288
Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly	
85 90 95	
TAC AGC TGG TAC AAA GGT GAA AGA GTG GAT GGC AAC CGT CAA ATT ATA	336
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile	
100 105 110	
GGA TAT GTA ATA GGA ACT CAA CAA GCT ACC CCA GGG CCC GCA TAC AGT	384

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Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser	
		115					120					125				
GGT	CGA	GAG	ATA	ATA	TAC	CCC	AAT	GCA	TCC	CTG	CTG	ATC	CAG	AAC	ATC	432
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile	
	130					135					140					
ATC	CAG	AAT	GAC	ACA	GGA	TTC	TAC	ACC	CTA	CAC	GTC	ATA	AAG	TCA	GAT	480
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp	
145					150					155					160	
CTT	GTG	AAT	GAA	GAA	GCA	ACT	GGC	CAG	TTC	CGG	GTA	TAC	CCG	GAG	CTG	528
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu	
				165					170					175		
CCC	AAG	CCC	TCC	ATC	TCC	AGC	AAC	AAC	TCC	AAA	CCC	GTG	GAG	GAC	AAG	576
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys	
			180					185					190			
GAT	GCT	GTG	GCC	TTC	ACC	TGT	GAA	CCT	GAG	ACT	CAG	GAC	GCA	ACC	TAC	624
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr	
		195					200					205				
CTG	TGG	TGG	GTA	AAC	AAT	CAG	AGC	CTC	CCG	GTC	AGT	CCC	AGG	CTG	CAG	672
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln	
	210					215					220					
CTG	TCC	AAT	GGC	AAC	AGG	ACC	CTC	ACT	CTA	TTC	AAT	GTC	ACA	AGA	AAT	720
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn	
225					230					235					240	
GAC	ACA	GCA	AGC	TAC	AAA	TGT	GAA	ACC	CAG	AAC	CCA	GTG	AGT	GCC	AGG	768
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg	
				245					250					255		
CGC	AGT	GAT	TCA	GTC	ATC	CTG	AAT	GTC	CTC	TAT	GGC	CCG	GAT	GCC	CCC	816
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro	
			260					265					270			
ACC	ATT	TCC	CCT	CTA	AAC	ACA	TCT	TAC	AGA	TCA	GGG	GAA	AAT	CTG	AAC	864
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn	
		275					280					285				
CTC	TCC	TGC	CAT	GCA	GCC	TCT	AAC	CCA	CCT	GCA	CAG	TAC	TCT	TGG	TTT	912
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe	
	290					295					300					
GTC	AAT	GGG	ACT	TTC	CAG	CAA	TCC	ACC	CAA	GAG	CTC	TTT	ATC	CCC	AAC	960
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn	
305					310					315					320	
ATC	ACT	GTG	AAT	AAT	AGT	GGA	TCC	TAT	ACG	TGC	CAA	GCC	CAT	AAC	TCA	1008
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser	
				325					330					335		
GAC	ACT	GGC	CTC	AAT	AGG	ACC	ACA	GTC	ACG	ACG	ATC	ACA	GTC	TAT	GCA	1056
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala	
			340					345					350			
GAG	CCA	CCC	AAA	CCC	TTC	ATC	ACC	AGC	AAC	AAC	TCC	AAC	CCC	GTG	GAG	1104
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	
		355					360					365				
GAT	GAG	GAT	GCT	GTA	GCC	TTA	ACC	TGT	GAA	CCT	GAG	ATT	CAG	AAC	ACA	1152
Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr	
	370					375					380					
ACC	TAC	CTG	TGG	TGG	GTA	AAT	AAT	CAG	AGC	CTC	CCG	GTC	AGT	CCC	AGG	1200
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	
385					390					395					400	

CTG	CAG	CTG	TCC	AAT	GAC	AAC	AGG	ACC	CTC	ACT	CTA	CTC	AGT	GTC	ACA	1248
Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr	
				405					410					415		
AGG	AAT	GAT	GTA	GGA	CCC	TAT	GAG	TGT	GGA	ATC	CAG	AAC	GAA	TTA	AGT	1296
Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser	
			420					425					430			
GTT	GAC	CAC	AGC	GAC	CCA	GTC	ATC	CTG	AAT	GTC	CTC	TAT	GGC	CCA	GAC	1344
Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	
		435					440					445				
GAC	CCC	ACC	ATT	TCC	CCC	TCA	TAC	ACC	TAT	TAC	CGT	CCA	GGG	GTG	AAC	1392
Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn	
	450					455					460					
CTC	AGC	CTC	TCC	TGC	CAT	GCA	GCC	TCT	AAC	CCA	CCT	GCA	CAG	TAT	TCT	1440
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	
465				470						475					480	
TGG	CTG	ATT	GAT	GGG	AAC	ATC	CAG	CAA	CAC	ACA	CAA	GAG	CTC	TTT	ATC	1488
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile	
				485					490					495		
TCC	AAC	ATC	ACT	GAG	AAG	AAC	AGC	GGA	CTC	TAT	ACC	TGC	CAG	GCC	AAT	1536
Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn	
			500					505					510			
AAC	TCA	GCC	AGT	GGC	CAC	AGC	AGG	ACT	ACA	GTC	AAG	ACA	ATC	ACA	GTC	1584
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val	
		515					520					525				
TCT	GCG	GAG	CTG	CCC	AAG	CCC	TCC	ATC	TCC	AGC	AAC	AAC	TCC	AAA	CCC	1632
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	
	530					535					540					
GTG	GAG	GAC	AAG	GAT	GCT	GTG	GCC	TTC	ACC	TGT	GAA	CCT	GAG	GCT	CAG	1680
Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln	
545				550						555					560	
AAC	ACA	ACC	TAC	CTG	TGG	TGG	GTA	AAT	GGT	CAG	AGC	CTC	CCA	GTC	AGT	1728
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser	
				565					570					575		
CCC	AGG	CTG	CAG	CTG	TCC	AAT	GGC	AAC	AGG	ACC	CTC	ACT	CTA	TTC	AAT	1776
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	
			580					585					590			
GTC	ACA	AGA	AAT	GAC	GCA	AGA	GCC	TAT	GTA	TGT	GGA	ATC	CAG	AAC	TCA	1824
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser	
		595					600					605				
GTG	AGT	GCA	AAC	CGC	AGT	GAC	CCA	GTC	ACC	CTG	GAT	GTC	CTC	TAT	GGG	1872
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly	
	610					615					620					
CCG	GAC	ACC	CCC	ATC	ATT	TCC	CCC	CCA	GAC	TCG	TCT	TAC	CTT	TCG	GGA	1920
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly	
625				630						635					640	
GCG	AAC	CTC	AAC	CTC	TCC	TGC	CAC	TCG	GCC	TCT	AAC	CCA	TCC	CCG	CAG	1968
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln	
				645					650					655		
TAT	TCT	TGG	CGT	ATC	AAT	GGG	ATA	CCG	CAG	CAA	CAC	ACA	CAA	GTT	CTC	2016
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu	
			660					665					670			
TTT	ATC	GCC	AAA	ATC	ACG	CCA	AAT	AAT	AAC	GGG	ACC	TAT	GCC	TGT	TTT	2064



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Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe	
	675						680					685				
GTC	TCT	AAC	TTG	GCT	ACT	GGC	CGC	AAT	AAT	TCC	ATA	GTC	AAG	AGC	ATC	2112
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile	
	690					695					700					
ACA	GTC	TCT	GCA	TCT	GGA	ACT	TCT	CCT	GGT	CTC	TCA	GCT	GGG	GCC	ACT	2160
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Pro	Gly	Leu	Ser	Ala	Gly	Ala	Thr	
705					710					715					720	
GTC	GGC	ATC	ATG	ATT	GGA	GTG	CTG	GTT	GGG	GTT	GCT	CTG	ATA			2202
Val	Gly	Ile	Met	Ile	Gly	Val	Leu	Val	Gly	Val	Ala	Leu	Ile			
				725					730							
TAGCAGCCCT	GGTGTAGT															2220

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 734 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg	Pro	Ala	Asp	Gln	Thr	Val	Thr	Ala	Ala	Leu	Thr	Lys	Arg	Ser	Trp	
1				5					10					15		
Asn	Ser	Ser	Thr	Ser	Pro	Gln	Arg	Arg	Thr	Glu	Gln	Thr	Ala	Glu	Thr	
			20					25					30			
Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln	
		35					40					45				
Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr	
	50					55					60					
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly	
65					70					75					80	
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly	
			85						90					95		
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile	
			100					105					110			
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser	
		115				120						125				
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile	
	130					135					140					
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp	
145					150					155					160	
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu	
			165					170						175		
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys	
			180					185					190			
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr	
		195					200					205				
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln	
	210					215						220				

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn  
 225 230 235 240  
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg  
 245 250 255  
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro  
 260 265 270  
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn  
 275 280 285  
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe  
 290 295 300  
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn  
 305 310 315 320  
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser  
 325 330 335  
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala  
 340 345 350  
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu  
 355 360 365  
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr  
 370 375 380  
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg  
 385 390 395 400  
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr  
 405 410 415  
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser  
 420 425 430  
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp  
 435 440 445  
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn  
 450 455 460  
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser  
 465 470 475 480  
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile  
 485 490 495  
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn  
 500 505 510  
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val  
 515 520 525  
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro  
 530 535 540  
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln  
 545 550 555 560  
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser  
 565 570 575  
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn  
 580 585 590

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Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser  
595 600 605

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly  
610 615 620

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly  
625 630 635 640

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln  
645 650 655

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu  
660 665 670

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe  
675 680 685

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile  
690 695 700

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr  
705 710 715 720

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile  
725 730

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGTGAATT CCTAATACGA CTACCTATAG GTTAAAACAG C

41

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGAACCCT CGAGACCCAT TATG

24

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
CCACCAAGTA CGTAACCACA TATGG 25

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
GTGAGGACTG CTGG 14

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
CACCCTGCC CTCGAGAAGC TCACTATTG 29

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
CACCCTGCC CTCGAGAAGC TCACTATTG 29